SEQUENCE LISTING

<110> SmithKline Beecham Corporation

<120> A Set of Ubiquitous Cellular Proteins
   Involved in Viral Life Cycle

<130> P51375

<140> Unassigned
<141> Herewith

<150> 60/410,460
<151> 2002-09-13

<160> 8

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 1270
<212> PRT
<213> Homo sapien

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                20   25   30
Lys Phe Met Cys Glu Val Gln Val Glu Gly Tyr Asn Tyr Thr Gly Met
        35   40   45
Gly Asn Ser Thr Asn Lys Lys Asp Ala Gln Ser Asn Ala Ala Arg Asp
        50   55   60
Phe Val Asn Tyr Leu Val Arg Ile Asn Glu Ile Lys Ser Glu Glu Val
65   70   75   80
Pro Ala Phe Gly Val Ala Ser Pro Pro Leu Thr Asp Thr Pro Asp
                85   90   95
Thr Thr Ala Asn Ala Glu Gly Asp Leu Pro Thr Thr Met Gly Gly Pro
                100   105   110
Leu Pro Pro His Leu Ala Leu Lys Ala Glu Asn Asn Ser Glu Val Gly
        115   120   125

1

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Ala Ser Gly Tyr Gly Val Pro Gly Pro Thr Trp Asp Arg Gly Ala Asn
    130                 135             140
Leu Lys Asp Tyr Tyr Ser Arg Lys Glu Glu Gln Glu Val Gln Ala Thr
145                 150             155                 160
Leu Glu Ser Glu Glu Val Asp Leu Asn Ala Gly Leu His Gly Asn Trp
                165             170             175
Thr Leu Glu Asn Ala Lys Ala Arg Leu Asn Gln Tyr Phe Gln Lys Glu
            180             185             190
Lys Ile Gln Gly Glu Tyr Lys Tyr Thr Gln Val Gly Pro Asp His Asn
        195             200             205
Arg Ser Phe Ile Ala Glu Met Thr Ile Tyr Ile Lys Gln Leu Gly Arg
    210             215             220
Arg Ile Phe Ala Arg Glu His Gly Ser Asn Lys Lys Leu Ala Ala Gln
225             230             235             240
Ser Cys Ala Leu Ser Leu Val Arg Gln Leu Tyr His Leu Gly Val Val
                245             250             255
Glu Ala Tyr Ser Gly Leu Thr Lys Lys Lys Glu Gly Glu Thr Val Glu
            260             265             270
Pro Tyr Lys Val Asn Leu Ser Gln Asp Leu Glu His Gln Leu Gln Asn
        275             280             285
Ile Ile Gln Glu Leu Asn Leu Glu Ile Leu Pro Pro Pro Glu Asp Pro
    290             295             300
Ser Val Pro Val Ala Leu Asn Ile Gly Lys Leu Ala Gln Phe Glu Pro
305             310             315             320
Ser Gln Arg Gln Asn Gln Val Gly Val Val Pro Trp Ser Pro Pro Gln
            325             330             335
Ser Asn Trp Asn Pro Trp Thr Ser Ser Asn Ile Asp Glu Gly Pro Leu
            340             345             350
Ala Phe Ala Thr Pro Glu Gln Ile Ser Met Asp Leu Lys Asn Glu Leu
            355             360             365
Met Tyr Gln Leu Glu Gln Asp His Asp Leu Gln Ala Ile Leu Gln Glu
        370             375             380
Arg Glu Leu Leu Pro Val Lys Lys Phe Glu Ser Glu Ile Leu Glu Ala
385             390             395             400
Ile Ser Gln Asn Ser Val Val Ile Arg Gly Ala Thr Gly Cys Gly
            405             410             415
Lys Thr Thr Gln Val Pro Gln Phe Ile Leu Asp Asp Phe Ile Gln Asn
            420             425             430
Asp Arg Ala Ala Glu Cys Asn Ile Val Val Thr Gln Pro Arg Arg Ile
        435             440             445
Ser Ala Val Ser Val Ala Glu Arg Val Ala Phe Glu Arg Gly Glu Glu
    450             455             460
Pro Gly Lys Ser Cys Gly Tyr Ser Val Arg Phe Glu Ser Ile Leu Pro
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2

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465                    470                 475                 480
Arg Pro His Ala Ser Ile Met Phe Cys Thr Val Gly Val Leu Leu Arg
            485             490             495
Lys Leu Glu Ala Gly Ile Arg Gly Ile Ser His Val Ile Val Asp Glu
            500             505             510
Ile His Glu Arg Asp Ile Asn Thr Asp Phe Leu Leu Val Val Leu Arg
            515             520             525
Asp Val Val Gln Ala Tyr Pro Glu Val Arg Ile Val Leu Met Ser Ala
        530         535             540
Thr Ile Asp Thr Ser Met Phe Cys Glu Tyr Phe Phe Asn Cys Pro Ile
545                 550             555             560
Ile Glu Val Tyr Gly Arg Thr Tyr Pro Val Gln Glu Tyr Phe Leu Glu
                565             570             575
Asp Cys Ile Gln Met Thr His Phe Val Pro Pro Pro Lys Asp Lys Lys
            580             585             590
Lys Lys Asp Lys Asp Asp Asp Gly Gly Glu Asp Asp Asp Ala Asn Cys
        595             600             605
Asn Leu Ile Cys Gly Asp Glu Tyr Gly Pro Glu Thr Arg Leu Ser Met
    610             615             620
Ser Gln Leu Asn Glu Lys Glu Thr Pro Phe Glu Leu Ile Glu Ala Leu
625                 630             635             640
Leu Lys Tyr Ile Glu Thr Leu Asn Val Pro Gly Ala Val Leu Val Phe
            645             650             655
Leu Pro Gly Trp Asn Leu Ile Tyr Thr Met Gln Lys His Leu Glu Met
            660             665             670
Asn Pro His Phe Gly Ser His Arg Tyr Gln Ile Leu Pro Leu His Ser
            675             680             685
Gln Ile Pro Arg Glu Glu Gln Arg Lys Val Phe Asp Pro Val Pro Val
    690             695             700
Gly Val Thr Lys Val Ile Leu Ser Thr Asn Ile Ala Glu Thr Ser Ile
705             710             715             720
Thr Ile Asn Asp Val Val Tyr Val Ile Asp Ser Cys Lys Gln Lys Val
            725             730             735
Lys Leu Phe Thr Ala His Asn Asn Met Thr Asn Tyr Ser Thr Val Trp
            740             745             750
Ala Ser Lys Thr Asn Leu Glu Gln Arg Lys Gly Arg Ala Gly Arg Ser
        755             760             765
Thr Ala Gly Phe Cys Phe His Leu Cys Ser Arg Ala Arg Phe Glu Arg
    770             775             780
Leu Glu Thr His Met Thr Pro Glu Met Phe Arg Thr Pro Leu His Glu
785             790             795             800
Ile Ala Leu Ser Ile Lys Leu Leu Arg Leu Gly Gly Ile Gly Gln Phe
            805             810             815
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3

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Leu Ala Lys Ala Ile Glu Pro Pro Pro Leu Asp Ala Val Ile Glu Ala
            820             825             830
Glu His Thr Leu Arg Glu Leu Asp Ala Leu Asp Ala Asn Asp Glu Leu
        835             840             845
Thr Pro Leu Gly Arg Ile Leu Ala Lys Leu Pro Ile Glu Pro Arg Phe
    850             855             860
Gly Lys Met Met Ile Met Gly Cys Ile Phe Tyr Val Gly Asp Ala Ile
865             870             875             880
Cys Thr Ile Ala Ala Ala Thr Cys Phe Pro Glu Pro Phe Ile Asn Glu
            885             890             895
Gly Lys Arg Leu Gly Tyr Ile His Arg Asn Phe Ala Gly Asn Arg Phe
        900             905             910
Ser Asp His Val Ala Leu Leu Ser Val Phe Gln Ala Trp Asp Asp Ala
        915             920             925
Arg Met Gly Gly Glu Glu Ala Glu Ile Arg Phe Cys Glu His Lys Arg
    930             935             940
Leu Asn Met Ala Thr Leu Arg Met Thr Trp Glu Ala Lys Val Gln Leu
945             950             955             960
Lys Glu Ile Leu Ile Asn Ser Gly Phe Pro Glu Asp Cys Leu Leu Thr
            965             970             975
Gln Val Phe Thr Asn Thr Gly Pro Asp Asn Asn Leu Asp Val Val Ile
        980             985             990
Ser Leu Leu Ala Phe Gly Val Tyr Pro Asn Val Cys Tyr His Lys Glu
        995             1000            1005
Lys Arg Lys Ile Leu Thr Thr Glu Gly Arg Asn Ala Leu Ile His Lys
    1010            1015            1020
Ser Ser Val Asn Cys Pro Phe Ser Ser Gln Asp Met Lys Tyr Pro Ser
1025            1030            1035            1040
Pro Phe Phe Val Phe Gly Glu Lys Ile Arg Thr Arg Ala Ile Ser Ala
            1045            1050            1055
Lys Gly Met Thr Leu Val Pro Pro Leu Gln Leu Leu Leu Phe Ala Ser
            1060            1065            1070
Lys Lys Val Gln Ser Asp Gly Gln Ile Val Leu Val Asp Asp Trp Ile
        1075            1080            1085
Lys Leu Gln Ile Ser His Glu Ala Ala Ala Cys Ile Thr Gly Leu Arg
    1090            1095            1100
Ala Ala Met Glu Ala Leu Val Val Glu Val Thr Lys Gln Pro Ala Ile
1105            1110            1115            1120
Ile Ser Gln Leu Asp Pro Val Asn Glu Arg Met Leu Asn Met Ile Arg
            1125            1130            1135
Gln Ile Ser Arg Pro Ser Ala Ala Gly Ile Asn Leu Met Ile Gly Ser
            1140            1145            1150
Thr Arg Tyr Gly Asp Gly Pro Arg Pro Pro Lys Met Ala Arg Tyr Asp
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4

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         1155                    1160                    1165
Asn Gly Ser Gly Tyr Arg Arg Gly Gly Ser Ser Tyr Ser Gly Gly Gly
     1170                    1175                    1180
Tyr Gly Gly Gly Tyr Ser Ser Gly Gly Tyr Gly Ser Gly Gly Tyr Gly
1185                    1190                    1195                    1200
Gly Ser Ala Asn Ser Phe Arg Ala Gly Tyr Gly Ala Gly Val Gly Gly
                1205                    1210                    1215
Gly Tyr Arg Gly Val Ser Arg Gly Gly Phe Arg Gly Asn Ser Gly Gly
                1220                    1225                    1230
Asp Tyr Arg Gly Pro Ser Gly Gly Tyr Arg Gly Ser Gly Gly Phe Gln
          1235                    1240                    1245
Arg Gly Gly Gly Arg Gly Ala Tyr Gly Thr Gly Tyr Phe Gly Gln Gly
     1250                    1255                    1260
Arg Gly Gly Gly Gly Tyr
1265                    1270
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<210> 2
<211> 3810
<212> DNA
<213> Home sapien

<400> 2
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tatgaaatta gagcagtggg gaacaaaaac aggcagaaat tcatgtgtga ggttcaggtg 120
gaaggttata attacactgg catgggaaat tccaccaata aaaaagatgc acaaagcaat 180
gctgccagag actttgttaa ctatttggtt cgaataaatg aaataaagag tgaagaagtt 240
ccagcttttg gggtagcatc tccgccccca cttactgata tcctgacac tacagcaaat 300
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gcagaaaata attctgaggt aggggcctct ggctatggtg ttcctgggcc cacctgggac 420
cgaggagcca acttgaagga ttactactca agaaaggaag aacaagaagt gcaagcgact 480
ctagaatcag aagaagtgga tttaaatgct gggcttcatg gaaactggac cttggaaaat 540
gctaaagctc gtctaaacca atattttcag aaagaaaaga tccaaggaga atataagtac 600
acccaagtgg gtcctgatca caacaggagc tttattgcag aaatgaccat ttatatcaag 660
cagctgggca gaaggatttt tgcacgagaa catggatcaa ataagaaatt ggcagcacag 720
tcctgtgccc tgtcacttgt cagacaactg taccatcttg gagtggttga gcttactcc 780
ggacttacaa agaagaagga aggagagaca gtggagcctt acaaagtaaa cctctctcaa 840
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cctgaagatc cttctgtgcc agttgcactc aacattggca aattggctca gttcgaacca 960
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ccttggacta gtagcaacat tgatgagggg cctctggctt ttgctactcc agagcaaata 1080
agcatggacc tcaagaatga attgatgtac cagttggaac aggatcatga tttgcaagca 1140
atcttgcagg agagagagtt actgcctgtg aagaaatttg aaagtgagat tctggaagca 1200
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atcagccaaa attcagttgt cattattaga ggggctactg gatgtgggaa aaccacacag 1260
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tacagaggat ctggggggatt ccagcgagga ggtggtaggg gggcctatgg aactggctac 3780
```

6

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<211> 894
<212> PRT
<213> Homo sapien

<400> 3
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Lys His Ser Ser Val Tyr Pro Thr Gln Glu Glu Leu Glu Ala Val Gln
            20   25   30

Asn Met Val Ser His Thr Glu Arg Ala Leu Lys Ala Val Ser Asp Trp
        35   40   45

Ile Asp Glu Gln Glu Lys Gly Ser Ser Glu Gln Ala Glu Ser Asp Asn
    50   55   60

Met Asp Val Pro Pro Glu Asp Asp Ser Lys Glu Gly Ala Gly Glu Gln
65   70   75   80

Lys Thr Glu His Met Thr Arg Thr Leu Arg Gly Val Met Arg Val Gly
                85   90   95

Leu Val Ala Lys Cys Leu Leu Leu Lys Gly Asp Leu Asp Leu Glu Leu
            100   105   .110

Val Leu Leu Cys Lys Glu Lys Pro Thr Thr Ala Leu Leu Asp Lys Val
        115   120   125

Ala Asp Asn Leu Ala Ile Gln Leu Ala Ala Val Thr Glu Asp Lys Tyr
    130   135   140

Glu Ile Leu Gln Ser Val Asp Asp Ala Ala Ile Val Ile Lys Asn Thr
145   150   155   160

Lys Glu Pro Pro Leu Ser Leu Thr Ile His Leu Thr Ser Pro Val Val
                165   170   175

Arg Glu Glu Met Glu Lys Val Leu Ala Gly Glu Thr Leu Ser Val Asn
            180   185   190

Asp Pro Pro Asp Val Leu Asp Arg Gln Lys Cys Leu Ala Ala Leu Ala
            195   200   205

Ser Leu Arg His Ala Lys Trp Phe Gln Ala Arg Ala Asn Gly Leu Lys
    210   215   220

Ser Cys Val Ile Val Ile Arg Val Leu Arg Asp Leu Cys Thr Arg Val
225   230   235   240

Pro Thr Trp Gly Pro Leu Arg Gly Trp Pro Leu Glu Leu Leu Cys Glu
                245   250   255

Lys Ser Ile Gly Thr Ala Asn Arg Pro Met Gly Ala Gly Glu Ala Leu
            260   265   270

Arg Arg Val Leu Glu Cys Leu Ala Ser Gly Ile Val Met Pro Asp Gly

7

```
           275                  280                  285
Ser Gly Ile Tyr Asp Pro Cys Glu Lys Glu Ala Thr Asp Ala Ile Gly
   290                  295                  300
His Leu Asp Arg Gln Gln Arg Glu Asp Ile Thr Gln Ser Ala Gln His
305                  310                  315                  320
Ala Leu Arg Leu Ala Ala Phe Gly Gln Leu His Lys Val Leu Gly Met
               325                  330                  335
Asp Pro Leu Pro Ser Lys Met Pro Lys Lys Pro Lys Asn Glu Asn Pro
               340                  345                  350
Val Asp Tyr Thr Val Gln Ile Pro Pro Ser Thr Thr Tyr Ala Ile Thr
               355                  360                  365
Pro Met Lys Arg Pro Met Glu Glu Asp Gly Glu Glu Lys Ser Pro Ser
           370                  375                  380
Lys Lys Lys Lys Lys Ile Gln Lys Lys Glu Glu Lys Ala Glu Pro Pro
385                  390                  395                  400
Gln Ala Met Asn Ala Leu Met Arg Leu Asn Gln Leu Lys Pro Gly Leu
               405                  410                  415
Gln Tyr Lys Leu Val Ser Gln Thr Gly Pro Val His Ala Pro Ile Phe
               420                  425                  430
Thr Met Ser Val Glu Val Asp Gly Asn Ser Phe Glu Ala Ser Gly Pro
           435                  440                  445
Ser Lys Lys Thr Ala Lys Leu His Val Ala Val Lys Val Leu Gln Asp
           450                  455                  460
Met Gly Leu Pro Thr Gly Ala Glu Gly Arg Asp Ser Ser Lys Gly Glu
465                  470                  475                  480
Asp Ser Ala Glu Glu Thr Glu Ala Lys Pro Ala Val Val Ala Pro Ala
               485                  490                  495
Pro Val Val Glu Ala Val Ser Thr Pro Ser Ala Ala Phe Pro Ser Asp
           500                  505                  510
Ala Thr Ala Glu Gln Gly Pro Ile Leu Thr Lys His Gly Lys Asn Pro
           515                  520                  525
Val Met Glu Leu Asn Glu Lys Arg Arg Gly Leu Lys Tyr Glu Leu Ile
           530                  535                  540
Ser Glu Thr Gly Gly Ser His Asp Lys Arg Phe Val Met Glu Val Glu
545                  550                  555                  560
Val Asp Gly Gln Lys Phe Gln Gly Ala Gly Ser Asn Lys Lys Val Ala
               565                  570                  575
Lys Ala Tyr Ala Ala Leu Ala Ala Leu Glu Lys Leu Phe Pro Asp Thr
           580                  585                  590
Pro Leu Ala Leu Asp Ala Asn Lys Lys Lys Arg Ala Pro Val Pro Val
       595                  600                  605
Arg Gly Gly Pro Lys Phe Ala Ala Lys Pro His Asn Pro Gly Phe Gly
   610                  615                  620
```

8

```
Met Gly Gly Pro Met His Asn Glu Val Pro Pro Pro Pro Asn Leu Arg
625                 630             635             '       640
Gly Arg Gly Arg Gly Gly Ser Ile Arg Gly Arg Gly Arg Gly Arg Gly
                645             650             655
Phe Gly Gly Ala Asn His Gly Gly Tyr Met Asn Ala Gly Ala Gly Tyr
            660             665             670
Gly Ser Tyr Gly Tyr Gly Gly Asn Ser Ala Thr Ala Gly Tyr Ser Gln
        675             680             685
Phe Tyr Ser Asn Gly Gly His Ser Gly Asn Ala Ser Gly Gly Gly Gly
        690             695             700
Gly Gly Gly Gly Gly Ser Ser Gly Tyr Gly Ser Tyr Tyr Gln Gly Asp
705             710             715             720
Asn Tyr Asn Ser Pro Val Pro Pro Lys His Ala Gly Lys Lys Gln Pro
            725             730             735
His Gly Gly Gln Gln Lys Pro Ser Tyr Gly Ser Gly Tyr Gln Ser His
            740             745             750
Gln Gly Gln Gln Gln Ser Tyr Asn Gln Ser Pro Tyr Ser Asn Tyr Gly
        755             760             765
Pro Pro Gln Gly Lys Gln Lys Gly Tyr Asn His Gly Gln Gly Ser Tyr
    770             775             780
Ser Tyr Ser Asn Ser Tyr Asn Ser Pro Gly Gly Gly Gly Gly Ser Asp
785             790             795             800
Tyr Asn Tyr Glu Ser Lys Phe Asn Tyr Ser Gly Ser Gly Gly Arg Ser
            805             810             815
Gly Gly Asn Ser Tyr Gly Ser Gly Gly Ala Ser Tyr Asn Pro Gly Ser
            820             825             830
His Gly Gly Tyr Gly Gly Gly Ser Gly Gly Gly Ser Ser Tyr Gln Gly
        835             840             845
Lys Gln Gly Gly Tyr Ser Gln Ser Asn Tyr Asn Ser Pro Gly Ser Gly
    850             855             860
Gln Asn Tyr Ser Gly Pro Pro Ser Ser Tyr Gln Ser Ser Gln Gly Gly
865             870             875             880
Tyr Gly Arg Asn Ala Asp His Ser Met Asn Tyr Gln Tyr Arg
            885             890
```

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<211> 2685
<212> DNA
<213> Homo sapien

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9

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cagagcccct acagcaacta tggccctcca cagggcaagc agaaaggcta taaccatgga 2340
caaggcagct actcctactc gaactcctac aactctcccg ggggcggggg cggatccgac 2400
tacaactacg agagcaaatt caactacagt ggtagtggag ccgaagcggg cgggaacagc 2460
tacggctcag gcggggcatc ctacaaccca gggtcacacg ggggctacgg cggaggttct 2520
ggggcggct cctcatacca aggcaaacaa ggaggctact cacagtcgaa ctacaactcc 2580
ccggggtccg gccagaacta cagtggccct cccagctcct accagtcctc acaaggcggc 2640
```

.

tatggcagaa acgcagacca cagcatgaac taccagtaca gataa   26

<210> 5
<211> 702
<212> PRT
<213> Homo sapien

<400> 5
Met Arg Pro Met Arg Ile Phe Val Asn Asp Asp Arg His Val Met Ala
 1   5   10   15
Lys His Ser Ser Val Tyr Pro Thr Gln Glu Glu Leu Glu Ala Val Gln
                20   25   30
Asn Met Val Ser His Thr Glu Arg Ala Leu Lys Ala Val Ser Asp Trp
            35   40   45
Ile Asp Glu Gln Glu Lys Gly Ser Ser Glu Gln Ala Glu Ser Asp Asn
    50   55   60
Met Asp Val Pro Pro Glu Asp Asp Ser Lys Glu Gly Ala Gly Glu Gln
65   70   75   80
Lys Thr Glu His Met Thr Arg Thr Leu Arg Gly Val Met Arg Val Gly
                85   90   95
Leu Val Ala Lys Cys Leu Leu Leu Lys Gly Asp Leu Asp Leu Glu Leu
            100   105   110
Val Leu Leu Cys Lys Glu Lys Pro Thr Thr Ala Leu Leu Asp Lys Val
            115   120   125
Ala Asp Asn Leu Ala Ile Gln Leu Ala Ala Val Thr Glu Asp Lys Tyr
    130   135   140
Glu Ile Leu Gln Ser Val Asp Asp Ala Ala Ile Val Ile Lys Asn Thr
145   150   155   160
Lys Glu Pro Pro Leu Ser Leu Thr Ile His Leu Thr Ser Pro Val Val
                165   170   175
Arg Glu Glu Met Glu Lys Val Leu Ala Gly Glu Thr Leu Ser Val Asn
            180   185   190
Asp Pro Pro Asp Val Leu Asp Arg Gln Lys Cys Leu Ala Ala Leu Ala
            195   200   205
Ser Leu Arg His Ala Lys Trp Phe Gln Ala Arg Ala Asn Gly Leu Lys
    210   215   220
Ser Cys Val Ile Val Ile Arg Val Leu Arg Asp Leu Cys Thr Arg Val
225   230   235   240
Pro Thr Trp Gly Pro Leu Arg Gly Trp Pro Leu Glu Leu Leu Cys Glu
                245   250   255
Lys Ser Ile Gly Thr Ala Asn Arg Pro Met Gly Ala Gly Glu Ala Leu
            260   265   270
Arg Arg Val Leu Glu Cys Leu Ala Ser Gly Ile Val Met Pro Asp Gly

11

```
                275                      280                      285
    Ser Gly Ile Tyr Asp Pro Cys Glu Lys Glu Ala Thr Asp Ala Ile Gly
        290                      295                      300
    His Leu Asp Arg Gln Gln Arg Glu Asp Ile Thr Gln Ser Ala Gln His
    305                      310                      315                320
    Ala Leu Arg Leu Ala Ala Phe Gly Gln Leu His Lys Val Leu Gly Met
                    325                      330                      335
    Asp Pro Leu Pro Ser Lys Met Pro Lys Lys Pro Lys Asn Glu Asn Pro
                    340                      345                      350
    Val Asp Tyr Thr Val Gln Ile Pro Pro Ser Thr Thr Tyr Ala Ile Thr
                    355                      360                      365
    Pro Met Lys Arg Pro Met Glu Glu Asp Gly Glu Glu Lys Ser Pro Ser
        370                      375                      380
    Lys Lys Lys Lys Lys Ile Gln Lys Lys Glu Glu Lys Ala Glu Pro Pro
    385                      390                      395                400
    Gln Ala Met Asn Ala Leu Met Arg Leu Asn Gln Leu Lys Pro Gly Leu
                    405                      410                      415
    Gln Tyr Lys Leu Val Ser Gln Thr Gly Pro Val His Ala Pro Ile Phe
                    420                      425                      430
    Thr Met Ser Val Glu Val Asp Gly Asn Ser Phe Glu Ala Ser Gly Pro
                    435                      440                      445
    Ser Lys Lys Thr Ala Lys Leu His Val Ala Val Lys Val Leu Gln Asp
        450                      455                      460
    Met Gly Leu Pro Thr Gly Ala Glu Gly Arg Asp Ser Ser Lys Gly Glu
    465                      470                      475                480
    Asp Ser Ala Glu Glu Thr Glu Ala Lys Pro Ala Val Val Ala Pro Ala
                    485                      490                      495
    Pro Val Val Glu Ala Val Ser Thr Pro Ser Ala Ala Phe Pro Ser Asp
                    500                      505                      510
    Ala Thr Ala Glu Gln Gly Pro Ile Leu Thr Lys His Gly Lys Asn Pro
                    515                      520                      525
    Val Met Glu Leu Asn Glu Lys Arg Arg Gly Leu Lys Tyr Glu Leu Ile
        530                      535                      540
    Ser Glu Thr Gly Gly Ser His Asp Lys Arg Phe Val Met Glu Val Glu
    545                      550                      555                560
    Val Asp Gly Gln Lys Phe Gln Gly Ala Gly Ser Asn Lys Lys Val Ala
                    565                      570                      575
    Lys Ala Tyr Ala Ala Leu Ala Ala Leu Glu Lys Leu Phe Pro Asp Thr
                    580                      585                      590
    Pro Leu Ala Leu Asp Ala Asn Lys Lys Lys Arg Ala Pro Val Pro Val
                    595                      600                      605
    Arg Gly Gly Pro Lys Phe Ala Ala Lys Pro His Asn Pro Gly Phe Gly
        610                      615                      620
```

12

```
Met Gly Gly Pro Met His Asn Glu Val Pro Pro Pro Asn Leu Arg
625             630             635             640
Gly Arg Gly Arg Gly Gly Ser Ile Arg Gly Arg Gly Arg Gly Arg Gly
            645             650             655
Phe Gly Gly Ala Asn His Gly Gly Tyr Met Asn Ala Gly Ala Gly Tyr
            660             665             670
Gly Ser Tyr Gly Tyr Gly Gly Asn Ser Ala Thr Ala Gly Tyr Ser Asp
            675             680             685
Phe Phe Thr Asp Cys Tyr Gly Tyr His Asp Phe Gly Ser Ser
    690             695             700
```

```
<210> 6
<211> 2107
<212> DNA
<213> Homo sapien

<400> 6
atgcgtccaa tgcgaatttt tgtgaatgat gaccgccatg tgatggcaaa gcattcttcc 60
gtttatccaa cacaagagga gctggaggca gtccagaaca tggtgtccca cacggagcgg 120
gcgctcaaag ctgtgtccga ctggatagac gagcaggaaa agggtagcag cgagcaggca 180
gagtccgata acatggatgt gcccccagag gacgacagta agaagggggc tggggaacag 240
aagacggagc acatgaccag aaccctgcgg ggagtgatgc gggtgggcct ggtggcaaag 300
tgcctcctac tcaagggggga cttggatctg gagctggtgc tgctgtgtaa ggagaagccc 360
acaaccgccc tcctggacaa ggtggccgac aacctggcca tccagcttgc tgctgtaaca 420
gaagacaagt acgaaatact gcaatctgtc gacgatgctg cgattgtgat aaaaaacaca 480
aaagagcctc cattgtccct gaccatccac ctgacatccc ctgttgtcag agaagaaatg 540
gagaaagtat tagctggaga aacgctatca gtcaacgacc ccccggacgt tctggacagg 600
cagaaatgcc ttgctgcctt ggcgtccctc cgacacgcca agtggttcca ggccagagcc 660
aacgggctga agtcttgtgt cattgtgatc cgggtcttga gggacctgtg cactcgcgtg 720
cccacctggg gtccctccg aggctggcct ctcgagctcc tgtgtgagaa atccattggc 780
acggccaaca accgatggg tgctggcgag ccctgcggga gagtgctgga gtgcctggcg 840
tcgggcatcg tgatgccaga tggttctggc atttatgacc cttgtgaaaa agaagccact 900
gatgctattg ggcatctaga cagacagcaa cggaagata tcacacagag tgcgcagcac 960
gcactgcggc tcgctgcctt cggccagctc cataaagtcc taggcatgga ccctctgcct 1020
tccaagatgc ccaagaaacc aaagaatgaa acccagtgg actacaccgt tcagatccca 1080
ccaagcacca cctatgccat tacgcccatg aaacgcccaa tggaggagga cggggaggag 1140
aagtcgccca gcaaaaagaa gaagaagatt cagaagaaag aggagaaggc agagcccccc 1200
caggctatga atgccctgat gcggttgaac cagctgaagc cagggctgca gtacaagctg 1260
gtgtcccaga ctgggcccgt ccatgccccc atctttacca tgtctgtgga ggttgatggc 1320
aattcattcg aggcctctgg gccctccaaa aagacggcca agctgcacgt ggccgttaag 1380
gtgttacagg acatgggctt gccgacgggt gctgaaggca gggactcgag caagggggag 1440
gactcggctg aggagaccga ggcgaagcca gcagtggtgg cccctgcccc agtggtagaa 1500
```

13

```
gctgtctcca cccctagtgc ggcctttccc tcagatgcca ctgccgagca ggggccgatc 1560
ctgacaaagc acggcaagaa cccagtcatg gagctgaacg agaagaggcg tgggctcaag 1620
tacgagctca tctccgagac cgggggcagc cacgacaagc gcttcgtcat ggaggtcgaa 1680
gtggatggac agaagttcca aggtgctggt tccaacaaaa aggtggcgaa ggcctacgct 1740
gctcttgctg ccctagaaaa gcttttccct gacacccctc gcccttgatg ccaacaaaaa 1800
gaagagagcc ccagtacccg tcagaggggg accgaaattt gctgctaagc cacataaccc 1860
tggcttcggc atgggaggcc ccatgcacaa cgaagtgccc ccacccccca accttcgagg 1920
gcggggaaga ggcgggagca tccggggacg agggcgcggg cgaggatttg gtggcgccaa 1980
ccatggaggc tacatgaatg ccggtgctgg gtatggaagc tatgggtacg gaggcaactc 2040
tgcgacagca ggctacagtg acttttttcac agactgctac ggctatcatg attttgggtc 2100
ttcctag                                                     2107
```

```
<210> 7
<211> 406
<212> PRT
<213> Homo sapien
```

```
<400> 7
Met Arg Gly Asp Arg Gly Arg Gly Arg Gly Gly Arg Phe Gly Ser Arg
1               5                   10                  15
Gly Gly Pro Gly Gly Gly Phe Arg Pro Phe Val Pro His Ile Pro Phe
            20                  25                  30
Asp Phe Tyr Leu Cys Glu Met Ala Phe Pro Arg Val Lys Pro Ala Pro
        35                  40                  45
Asp Glu Thr Ser Phe Ser Glu Ala Leu Leu Lys Arg Asn Gln Asp Leu
    50                  55                  60
Ala Pro Asn Ser Ala Glu Gln Ala Ser Ile Leu Ser Leu Val Thr Lys
65                  70                  75                  80
Ile Asn Asn Val Ile Asp Asn Leu Ile Val Ala Pro Gly Thr Phe Glu
                85                  90                  95
Val Gln Ile Glu Glu Val Arg Gln Val Gly Ser Tyr Lys Lys Gly Thr
            100                 105                 110
Met Thr Thr Gly His Asn Val Ala Asp Leu Val Val Ile Leu Lys Ile
        115                 120                 125
Leu Pro Thr Leu Glu Ala Val Ala Ala Leu Gly Asn Lys Val Val Glu
    130                 135                 140
Ser Leu Arg Ala Gln Asp Pro Ser Glu Val Leu Thr Met Leu Thr Asn
145                 150                 155                 160
Glu Thr Gly Phe Glu Ile Ser Ser Ser Asp Ala Thr Val Lys Ile Leu
                165                 170                 175
Ile Thr Thr Val Pro Pro Asn Leu Arg Lys Leu Asp Pro Glu Leu His
            180                 185                 190
Leu Asp Ile Lys Val Leu Gln Ser Ala Leu Ala Ala Ile Arg His Ala
```

14

```
          195                    200                    205
Arg Trp Phe Glu Glu Asn Ala Ser Gln Ser Thr Val Lys Val Leu Ile
    210                    215                    220
Arg Leu Leu Lys Asp Leu Arg Ile Arg Phe Pro Gly Phe Glu Pro Leu
225                    230                    235                    240
Thr Pro Trp Ile Leu Asp Leu Leu Gly His Tyr Ala Val Met Asn Asn
                   245                    250                    255
Pro Thr Arg Gln Pro Leu Ala Leu Asn Val Ala Tyr Arg Arg Cys Leu
                260                    265                    270
Gln Ile Leu Ala Ala Gly Leu Phe Leu Pro Gly Ser Val Gly Ile Thr
          275                    280                    285
Asp Pro Cys Glu Ser Gly Asn Phe Arg Val His Thr Val Met Thr Leu
    290                    295                    300
Glu Gln Gln Asp Met Val Cys Tyr Thr Ala Gln Thr Leu Val Arg Ile
305                    310                    315                    320
Leu Ser His Gly Gly Phe Arg Lys Ile Leu Gly Gln Glu Gly Asp Ala
                325                    330                    335
Ser Tyr Leu Ala Ser Glu Ile Ser Thr Trp Asp Gly Val Ile Val Thr
          340                    345                    350
Pro Ser Glu Lys Ala Tyr Glu Lys Pro Pro Glu Lys Lys Glu Gly Glu
          355                    360                    365
Glu Glu Glu Glu Asn Thr Glu Arg Thr Thr Ser Arg Arg Gly Arg Arg
    370                    375                    380
Lys His Gly Asn Ser Gly Val Thr Phe Pro Ser Leu Leu Phe Leu Pro
385                    390                    395                    400
Lys Gly Lys Thr Gly Ala
                405
```

```
<210> 8
<211> 1221
<212> DNA
<213> Homo sapien
```

```
<400> 8
atgagggggtg acagaggccg tggtcgtggt gggcgctttg gttccagagg aggcccagga  60
ggagggttca ggccctttgt accacatatc ccatttgact tctatttgtg tgaaatggcc  120
tttccccggg tcaagccagc acctgatgag acttccttca gtgaggcctt gctgaagagg  180
aaccaggacc tggctcccaa ttctgctgaa caggcatcta tcctttctct agtgacaaaa  240
ataaacaatg tgattgataa tctgattgtg gctccaggga catttgaagt gcaaattgaa  300
gaagttcgac aggtgggatc ctataaaaag gggacaatga ctacaggaca caatgtggct  360
gacctggtgg tgatactcaa gattctgcca acgttggaag ctgttgctgc cctggggaac  420
aaagtcgtgg aaagcctaag agcacaggat ccttctgaag ttttaaccat gctgaccaac  480
```

```
gaaacaggct ttgaaatcag ttcttctgat gctacagtga agattctcat tacaacagtg 540
ccacccaatc ttcgaaaact ggatccagaa ctccatttgg atatcaaagt attgcagagt 600
gccttagcag ccatccgaca tgcccgctgg ttcgaggaaa atgcttctca gtccacagtt 660
aaagttctca tcagactact gaaggacttg aggattcgtt ttcccggctt tgagcccctc 720
acaccctgga tccttgacct actaggccat tatgctgtga tgaacaaccc caccagacag 780
cctttggccc taaacgttgc atacaggcgc tgcttgcaga ttctggctgc aggactgttc 840
ctgccaggtt cagtgggtat cactgacccc tgtgagagtg gcaactttag agtacacaca 900
gtcatgaccc tagaacagca ggacatggtc tgctatacag ctcagactct cgtccgaatc 960
ctctcacatg gtggctttag gaagatcctt ggccaggagg gtgatgccag ctatcttgct 1020
tctgaaatat ctacctggga tggagtgata gtaacacctt cagaaaaggc ttatgagaag 1080
ccaccagaga agaaggaagg agaggaagaa gaggagaata cagaaagaac cacctcaagg 1140
agaggaagaa gaaagcatgg aaactcagga gtgacattcc cttcactcct tttcctaccc 1200
aagggaaaga ctggagccta a                                             1221
```